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The physiological consequences of an activation of the immune system in fish are poorly understood. To assess the in vivo effects of lipopolysaccharide (LPS) on rainbow trout (*Oncorhyncus mykiss*) skeletal muscle function, we have performed genomic and proteomic analyses. We have examined changes in gene expression in white muscle (WM) and red muscle (RM) at 24 and 72 h after LPS treatment (6 mg/kg i.p.) by microarray analysis and in protein expression in WM at 24 h after challenge. As expected, LPS provokes changes in skeletal muscle gene and protein expression pattern. At the transcriptional level we show important changes in metabolic, mitochondrial and structural genes in both muscle types according to its function. In RM (an aerobic tissue that obtains energy mainly from oxidative phosphorylation) LPS provokes marked changes in representative mitochondrial genes. In contrast, WM (an anaerobic tissue) suffers major expression changes in glycolytic enzymes. Moreover, we observed a common immune response of whole skeletal muscle showing an increase in the expression of the antigen-presenting machinery. At the protein level we have evaluated the LPS effects on the proteomic expression pattern in WM. Fourteen spots differentially expressed by LPS treatment were identified, being mainly enzymes of glycolytic metabolism. Interestingly, we have found differences between protein and mRNA expression patterns suggesting the need to integrate both measures for a more complete understanding of gene expression in fish during LPS challenge. In summary, we have shown that LPS causes important changes in gene and protein expression in trout skeletal muscle, which can be indicative of potential detrimental effects of pathogen infection on growth and metabolic processes in fish.

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Growth improvement of Eurasian perch (*Perca fluviatilis*) using domesticated strains under intensive rearing conditions

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Since many years, selection and domestication programs in aquaculture allowed the improvement of growth performances, survival, quality and diseases resistance of many cultured fish species. The aim of the study was to compare, under intensive rearing conditions, the growth performances of different levels of domesticated and wild Eurasian perch, a new species in commercial activity. Weaned domesticated F_2 and F_4 juveniles (MBW = 500 mg, 58 days post-hatching) originated from captive breeders reared into a recirculating aquaculture system with a natural thermal-like cycle (4 to 26 °C), while wild juveniles originated from eggs ribbon collected in the wild (Robertville Lake, Belgium). Three generations of Eurasian perch juveniles (wild, F_2 and F_4) were reared in duplicate during 250 days into 1.6 m^3/4 m^2 tanks (initial stocking densities: 3125) in a recirculating system at 23 °C (O_2 > 6 ppm). All fish were counted and biomass measured every 2 weeks in order to calculate survival rate and to adapt food ration. Individual growth was measured every month on 50 fish per generation. After a 250 day rearing period, growth performances were significantly improved (45%) with domesticated strains (MBW = 113.5 and 100.4 g for F_2 and F_4 respectively and 60.0 g for the wild strain). The food conversion ratio was also better for the domesticated strains (0.9 and 1.1 for F_2 and F_4, respectively and 1.3 for the wild strain). These results suggested that the domestication program of Eurasian perch allows the improvement of growth performances and productivity of this species reared under intensive conditions.

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Sex determination in Nile tilapia, *Oreochromis niloticus*: Effect of high temperature during embryogenesis on sex ratio and sex differentiation pathway

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Sex differentiation in fish is under the control of genetic (GSD) and environmental (ESD) factors. Generally, environmental factors, mainly temperature (TSD), act on sex differentiation pathway after hatching, during the gonadal development, but few are known about their role during embryogenesis, before the onset of the gonadogenesis. The aim of the study was to